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7751 CACCCAAGGA AGTTATGTGG TTAATTGTAA TACCAAAAAA CCAAACCTGG
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7951 TTCAAGCCCA CAATTTGGCT CACACCGGAC GTGAAGCCAC TCTTTTAAA
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8001 ATTGCCAACC TTTATTGGTG GCCAAATATG AGAAAGGATG TGGTTAAACA
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SEQ ID NO: 3

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QNKSKKKAQQAADTGNN SQVSQNYPIVQNLQGQMVHQAI SPRTLNAWVKV
VEEKAFSPEVIPMFSA LSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAE
WDR LHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNPPIPVGEIYKR
WILGLNKIVRMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMT
ETLLVQANANPDCKTILKALGPATLEEMMTACQGVGGPGHKARVLAEAMSQ
VTNPATIMI QKGNFRNQ RKT V KCFNCGKEGHI AKNCRAPRKKGCWKCGKEGH
QMKDCTERQANFLGKI WPSHKGRPGNFLQSRPEPTAPPEESFRFGEETTPSQK
QEPIDKELYPLASLRSLFGSDPSSQ

SEQ ID NO: 4

MGARASVLSGGELDRWEKIRLRPGGKKKYK LKHIVWASRELERFAVNPGLLE
TSEGC RQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEE
QNKSKKKAQQAADTG HSSQVSQNYPIVQNIQGQMVHQAI SPRTLNAWVKV
VEEKAFSPEVIPMFSA LSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAE
WDRVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNPPIPVGEIYKR
WILGLNKIVRMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMT
ETLLVQANANPDCKTILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQ
VTNSATIMMQRGNFRNQ RKIVKCFNCGKEGHI ARNCRAPRKKGCWKCGKEG
HQM K DCTERQANFLGKI WPSYKGRPGNFLQSRPEPTAPPFLQSRPEPTAPPEES
FRSGVETTPSQKQEPIDKELYPLTSLRSLFGNDPSSQ

SEQ ID NO: 5

MGARASVLSGGELDRWEKVRLRPGGKKKYK LKHIVWASRELERFAVNPGLLE
TSEGC RQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEE
QNKSKKKAQQAADTG HSSQVSQNYPIVQNIQGQMVHQAI SPRTLNAWVKV
VEEKAFSPEVIPMFSA LSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAE
WDRVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNPPIPVGEIYKR
WILGLNKIVRMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMT
ETLLVQANANPDCKTILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQ
VTNSATIMMQRGNFRNQ RKIVKCFNCGKEGHI ARNCRAPRKKGCWKCGKEG
HQM K DCTERQANFLGKI WPSYKGRPGNFLQSRPEPTAPPFLQSRPEPTAPPEES
FRSGVETTPSQKQEPIDKELYPLTSLRSLFGNDPSSQ

SEQ ID NO: 6

TCC GGG CCC GGA ATG CCT ATA GTC CAG AAC ATC C

SEQ ID NO: 7

GCG GCC GCG TTT TGA GAA CGA AAT ACC GG

SEQ ID NO: 8

SEQ ID NO:1 with SEQ ID NO: 2 inserted between 12816 and 13552.